

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:38:08 ; Search time 57 Seconds
(without alignments)
7401.817 Million cell updates/sec

Title: US-10-090-183-6

Perfect score: 7046

Sequence: 1 MESKALLAVALMFCVETRAA.....KMWDAVAHADSGTTLRSPV 1345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7046	100.0	1345	14	US-10-090-183-6
2	7020	99.6	1367	9	US-09-766-678-2
3	7020	99.6	1367	15	US-10-165-193A-10
4	6994	99.3	1367	9	US-09-919-408-6
5	6994	99.3	1367	9	US-09-872-136-6
6	6127.5	87.0	1356	14	US-10-024-939-2
7	6127.5	87.0	1356	14	US-10-100-405A-2
8	6127.5	87.0	1356	14	US-10-327-414-6
9	6127.5	87.0	1356	15	US-10-165-193A-11
10	6124.5	86.9	1356	15	US-10-090-183-2
11	6124.5	86.9	1356	15	US-10-394-322A-66
12	6124.5	86.9	1356	15	US-10-440-464-129
13	6123.5	86.9	1356	10	US-09-969-037-7
14	6092.5	86.5	1354	14	US-10-262-538-30
15	4228	60.0	806	9	US-09-766-678-5

16	4196	59.6	805	13	US-10-036-869-34	Sequence 34, Appl
17	3851	54.7	731	14	US-10-364-949-2	Sequence 2, Appl
18	3343	47.4	789	14	US-10-101-018-15	Sequence 15, Appl
19	3283	46.6	773	14	US-10-364-949-4	Sequence 4, Appl
20	3245	46.1	767	14	US-10-105-901-2	Sequence 2, Appl
21	3240	46.0	764	14	US-10-091-300-85	Sequence 85, Appl
22	3143	44.6	942	16	US-10-449-609-8	Sequence 34, Appl
23	3126	44.4	738	14	US-10-425-668-34	Sequence 13, Appl
24	2792	39.6	664	14	US-10-101-018-13	Sequence 8, Appl
25	2764.5	39.2	567	14	US-10-327-414-8	Sequence 19, Appl
26	2746.5	39.0	1363	10	US-09-375-248-19	Sequence 19, Appl
27	2746.5	39.0	1363	12	US-10-661-740-19	Sequence 34, Appl
28	2733.5	38.8	1368	14	US-10-105-901-34	Sequence 215, Appl
29	2694.5	38.2	1338	12	US-10-211-462-215	Sequence 23, Appl
30	2694.5	38.2	1338	12	US-10-060-065-23	Sequence 44, Appl
31	2694.5	38.2	1338	14	US-10-059-585-44	Sequence 84, Appl
32	2694.5	38.2	1338	14	US-10-021-660-84	Sequence 26, Appl
33	2694.5	38.2	1338	16	US-10-621-116-26	Sequence 4, Appl
34	2692.5	38.2	1338	14	US-10-090-183-4	Sequence 129, Appl
35	2692.5	38.2	1338	15	US-10-116-275-129	Sequence 33, Appl
36	2691.5	38.2	1362	14	US-10-105-901-33	Sequence 2, Appl
37	2688	38.1	1339	15	US-10-165-193A-9	Sequence 2, Appl
38	2682	38.1	1363	10	US-09-375-248-2	Sequence 4, Appl
39	2682	38.1	1363	12	US-09-765-534B-4	Sequence 2, Appl
40	2682	38.1	1363	12	US-10-661-740-2	Sequence 33, Appl
41	2677.5	38.0	1298	9	US-09-982-610-33	Sequence 2, Appl
42	2677.5	38.0	1298	12	US-09-765-534B-2	Sequence 32, Appl
43	2677.5	38.0	1298	14	US-10-262-538-32	Sequence 67, Appl
44	2677.5	38.0	1298	15	US-10-394-322A-67	Sequence 5, Appl
45	2672.5	37.9	1311	12	US-09-765-534B-5	

ALIGNMENTS

RESULT 1
US-10-090-183-6
; Sequence 6, Application US/10090183
; Publication No. US20030185802A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Ralph A. Reisfeld
; APPLICANT: Andrew G. Niethammer
; APPLICANT: Rong Xiang
; TITLE OF INVENTION: DNA VACCINE AGAINST PROLIFERATING
; TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-829.0
; CURRENT APPLICATION NUMBER: US/10/090,183
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1345
; TYPE: PRT
; ORGANISM: mouse
US-10-090-183-6

Query Match 100.0%; Score 7046; DB 14; Length 1345;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MESKALLAVALMFCVETRAASVGLTFLHPPKLSQDKDILTLANTTLQITCRGORDLD	60
DB	1	MESKALLAVALMFCVETRAASVGLTFLHPPKLSQDKDILTLANTTLQITCRGORDLD	60
QY	61	WLWPNQADSRERVLVTECGGSDSIFCKTLTIPRVVGNDTGAYKGSYRDVDTASTVYVYV	120
DB	61	WLWPNQADSRERVLVTECGGSDSIFCKTLTIPRVVGNDTGAYKGSYRDVDTASTVYVYV	120
QY	121	RDYRSPFIASVSDQHGIVYITENKNTVVIPTCRGISNLNLSLCARYPEKRFVPGNRTS	180
DB	121	RDYRSPFIASVSDQHGIVYITENKNTVVIPTCRGISNLNLSLCARYPEKRFVPGNRTS	180

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	7020	99.6	1367	2	US-08-443-861-2	Sequence 2, Appli
2	7020	99.6	1367	3	US-08-193-8298-2	Sequence 2, Appli
3	6994	99.3	1367	1	US-07-813-593-4	Sequence 4, Appli
4	6994	99.3	1367	1	US-07-977-451-6	Sequence 6, Appli
5	6994	99.3	1367	1	US-07-946-507-4	Sequence 4, Appli
6	6994	99.3	1367	1	US-08-252-517-6	Sequence 6, Appli
7	6994	99.3	1367	1	US-07-906-397A-6	Sequence 6, Appli
8	6994	99.3	1367	1	US-08-601-891-6	Sequence 6, Appli
9	6994	99.3	1367	2	US-09-021-324-6	Sequence 6, Appli
10	6994	99.3	1367	4	US-09-872-1368-6	Sequence 6, Appli
11	6994	99.3	1367	5	PCR-US92-02750-8	Sequence 8, Appli
12	6994	99.3	1367	5	PCR-US92-05401-6	Sequence 6, Appli
13	6994	99.3	1367	5	PCR-US92-09893-6	Sequence 6, Appli
14	6127.5	87.0	1356	3	US-09-098-707A-2	Sequence 2, Appli
15	6127.5	87.0	1356	4	US-09-483-539-2	Sequence 2, Appli
16	6102.5	86.6	1356	1	US-08-810-116-8	Sequence 8, Appli
17	6102.5	86.6	1356	2	US-07-930-548A-8	Sequence 8, Appli
18	4228	60.0	806	2	US-08-443-861-5	Sequence 5, Appli
19	4228	60.0	806	3	US-08-193-8298-5	Sequence 5, Appli
20	4196	59.6	805	3	US-08-985-526-34	Sequence 34, Appli
21	3327.5	47.2	788	1	US-08-232-538-15	Sequence 15, Appli
22	3327.5	47.2	788	2	US-08-786-164-15	Sequence 15, Appli
23	3248	46.1	764	4	US-09-142-9568-14	Sequence 14, Appli
24	3245	46.1	767	2	US-08-874-678-2	Sequence 2, Appli
25	3245	46.1	767	3	US-08-643-839-2	Sequence 2, Appli
26	3245	46.1	767	4	US-09-348-886-2	Sequence 2, Appli
27	2792	39.6	668	1	US-08-232-538-13	Sequence 13, Appli

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:34:27 ; Search time 21 Seconds
(without alignments)
6160.838 Million cell updates/sec

Title: US-10-090-183-6
Perfect score: 7046
Sequence: 1 MESKALLAVALWFCVETRAA.....KMWDAVHADSGTILRSPPV 1345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6998	99.3	1367	2 A41228	protein-tyrosine k
2	6102.5	86.6	1356	2 JCI402	protein-tyrosine k
3	4810.5	68.3	1348	2 S1656	vascular endotheli
4	2913	41.3	1379	2 J4954	vascular endotheli
5	2746.5	39.0	1363	2 I58375	protein-tyrosine k
6	2694.5	38.2	1338	2 S09982	protein-tyrosine k
7	2677.5	38.0	1298	2 A48999	protein-tyrosine k
8	2606	37.0	1336	2 I60598	Fit-1 tyrosine kin
9	2575	36.5	1333	2 I78875	receptor tyrosine
10	2524.5	35.8	1330	2 S49010	embryonic receptor
11	1162.5	16.5	1088	1 PRTGA	platelet-derived g
12	1162	16.5	1089	1 PFHUGA	platelet-derived g
13	1142	16.2	1089	1 S33727	platelet-derived g
14	1130.5	16.0	1087	2 I51552	platelet-derived g
15	1077.5	15.3	975	2 T30816	macrophage colony-
16	1049.5	14.9	1048	2 T30815	platelet-derived g
17	1043.5	14.8	960	1 JN0677	protein-tyrosine k
18	1019.5	14.5	976	1 TVHUKT	protein-tyrosine k
19	1019	14.5	978	1 A49814	protein-tyrosine k
20	1019	14.5	1106	1 PFHUGB	platelet-derived g
21	1016.5	14.4	975	1 TWMSKT	protein-tyrosine k
22	1009	14.3	977	2 I45877	protein-tyrosine k
23	1003	14.2	806	2 A35963	platelet-derived g
24	1000.5	14.2	1098	1 PWSRB	platelet-derived g
25	999.5	14.2	819	1 TVCHFG	fibroblast growth
26	994	14.1	980	1 TVCTMD	macrophage colony-
27	993.5	14.1	816	2 A49151	fibroblast growth
28	992	14.1	814	1 A39752	fibroblast growth
29	992	14.1	821	1 TWMSBK	fibroblast growth

ALIGNMENTS

RESULT 1

A41228
protein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recept
C:Species: Mus musculus (house mouse)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 04-Feb-2000
C:Accession: A41228; A46065; I58365; S18832; S29991
R:Matthews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.
Proc. Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991
A:Title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitive
A:Reference number: A41228; MUID:92020984; PMID:1717995
A:Accession: A41228
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1367 <WAT>
A:Cross-references: GB:X59397; NID:G50976; PIDN:CAA42040.1; PID:G50977
R:Millauer, B.; Witzmann-Voos, S.; Schurch, H.; Martinez, R.; Moller, N.P.; Risau, W.;
Cell 72, 835-846, 1993
A:Title: High affinity VEGF binding and developmental expression suggest Flk-1 as a major
A:Reference number: A46065; MUID:93208880; PMID:7681362
A:Accession: A46065
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-24, 'T', '26-782', 'VL', '785-916', 'C', '918-1367' <MIL>
A:Cross-references: GB:X70842; NID:G57923; PIDN:CAA50192.1; PID:G57924
A:Note: submitted to the EMBL Data Library, January 1993
A:Note: sequence extracted from NCBI backbone (NCBIP:128064)
R:Oelrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemielski, A.; Wilks, A.F.
Oncogene 8, 11-18, 1993
A:Title: NYK/Flk-1: a putative receptor protein tyrosine kinase isolated from E10 embryo
A:Reference number: I58365; MUID:93141255; PMID:8423988
A:Accession: I58365
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-678, 'D', '680-1340', 'RSPPV' <OEL>
A:Cross-references: GB:S53103; NID:G264004; PIDN:AAB25043.1; PID:G264005
C:Genetics:
A:Gene: FLK-1; NYK
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane f
P:830-1165/Domain: protein kinase homology <KIN>
P:838-846/Region: protein kinase ATP-binding motif
Query Match 99.3%; Score 5998; DB 2; Length 1367;
Best Local Similarity 99.6%; Pred. No. 5.5e-302;
Matches 1336; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MESKALLAVALWFCVETRAASVGLTGDFLHPKLSKTDILTILANTTLQITCRQRDL 60
Db 1 MESKALLAVALWFCVETRAASVGLTGDFLHPKLSKTDILTILANTTLQITCRQRDL 60
Qy 61 WLWPNQARDSEERVLVTECGGDSIFCKTLTIPRVGNDTGAYKCSYRDVDIASTVYVV 120

Db 61 WLWPNQADSRBRLVTBCCGGDSIPCKTLTIPRVVGNNTGAYKCSYRDVDIASTVYVVV 120
Qy 121 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIENLVSLCARYPEKRVFVPGNRLS 180
Db 121 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIENLVSLCARYPEKRVFVPGNRLS 180
Qy 181 WDSIEGFTLPSPYMSIYAGVWFCPEAKINDETYQSIIMYIVVVGRIYDVVILSPHIELSA 240
Db 181 WDSIEGFTLPSPYMSIYAGVWFCPEAKINDETYQSIIMYIVVVGRIYDVVILSPHIELSA 240
Qy 241 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPPGTVAKMFLSTLTIESVT 300
Db 241 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPPGTVAKMFLSTLTIESVT 300
Qy 301 KSDQGEYTCVASSGRMIKNRRTFVRVHTKPTAFAGSGMSLVEATVGSQVRIPVKLSYP 360
Db 301 KSDQGEYTCVASSGRMIKNRRTFVRVHTKPTAFAGSGMSLVEATVGSQVRIPVKLSYP 360
Qy 361 APDIKWYRNGRPISNYTMIVGDELTIMEVTERDAGNYTVILTNPISMEKQSHWVSLVN 420
Db 361 APDIKWYRNGRPISNYTMIVGDELTIMEVTERDAGNYTVILTNPISMEKQSHWVSLVN 420
Qy 421 VPPQIGEKALISPMDSYQGTWTLCTVYANPPLHHIQWYQLEBACSYRPGQTSFYAC 480
Db 421 VPPQIGEKALISPMDSYQGTWTLCTVYANPPLHHIQWYQLEBACSYRPGQTSFYAC 480
Qy 481 KSWRHVEDFQGGNKIEVTNNOVALIEGKNKTVSTLVIQANVSALYKCAINKAGRGV 540
Db 481 KSWRHVEDFQGGNKIEVTNNOVALIEGKNKTVSTLVIQANVSALYKCAINKAGRGV 540
Qy 541 ISFHVIRGPEITVQAAQTEQESVLLCTADRNTPENLTWYKLGSOATSVHMGSLTPV 600
Db 541 ISFHVIRGPEITVQAAQTEQESVLLCTADRNTPENLTWYKLGSOATSVHMGSLTPV 600
Qy 601 CKNLDAWKLNGTMSNSTNDILIVAFONASLODQGYVCSAQDKTKKRGHCLVKQLIIL 660
Db 601 CKNLDAWKLNGTMSNSTNDILIVAFONASLODQGYVCSAQDKTKKRGHCLVKQLIIL 660
Qy 661 ERWAPMITGNLENQTTIGETIEVTCPASGNPPTHTWPKDNETLVEDSGIVLRDGNRL 720
Db 661 ERWAPMITGNLENQTTIGETIEVTCPASGNPPTHTWPKDNETLVEDSGIVLRDGNRL 720
Qy 721 TIIRVRKEGGLYTCQACNVLCARAEITLFIIEGAQKTNLEVIILVGTAVIAMFFMLLL 780
Db 721 TIIRVRKEGGLYTCQACNVLCARAEITLFIIEGAQKTNLEVIILVGTAVIAMFFMLLL 780
Qy 781 VILVTVKRANEGELKTGYLSIVMDPDELPLDRCERLPLDYASKWBFPRDLKLGKPLGR 840
Db 781 VILVTVKRANEGELKTGYLSIVMDPDELPLDRCERLPLDYASKWBFPRDLKLGKPLGR 840
Qy 841 GAFQGVIEADAFGIDKTATCKTVAKMLKEGATHSEHRLMSLKITLIHGHILNVNLL 900
Db 841 GAFQGVIEADAFGIDKTATCKTVAKMLKEGATHSEHRLMSLKITLIHGHILNVNLL 900
Qy 901 GACTKPGGLWTVFCKGNLSTYLRKNEFPVYKSGARPGQKDYVGLSVDLKRR 960
Db 901 GACTKPGGLWTVFCKGNLSTYLRKNEFPVYKSGARPGQKDYVGLSVDLKRR 960
Qy 961 LDSITSSQSSAGSFVEKSLSDVBEESAEELYKDFLTLEHLICYSFQVAKGMEFLASR 1020
Db 961 LDSITSSQSSAGSFVEKSLSDVBEESAEELYKDFLTLEHLICYSFQVAKGMEFLASR 1020
Qy 1021 KCIHRLAARNILLSKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRYV 1080
Db 1021 KCIHRLAARNILLSKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRYV 1080
Qy 1081 TTQSDVMSFGVLWEIIFSLGASYPGVKIDEEFCRLKEGTRMRAPDYTPPENYQTMALC 1140
Db 1081 TTQSDVMSFGVLWEIIFSLGASYPGVKIDEEFCRLKEGTRMRAPDYTPPENYQTMALC 1140
Qy 1141 WHBDPNQRFPSFSELVHGLNLLQANAQDQKDYIVLPMSETLSMEEDSGLSLTPSVSCM 1200
Db 1141 WHBDPNQRFPSFSELVHGLNLLQANAQDQKDYIVLPMSETLSMEEDSGLSLTPSVSCM 1200

Qy 1201 EEEVCDPKFYNDTAGISHYLQNSKRKRPVSVKTFEDIPLEBPVKVIPDDSQTDSCM 1260
Db 1201 EEEVCDPKFYNDTAGISHYLQNSKRKRPVSVKTFEDIPLEBPVKVIPDDSQTDSCM 1260
Qy 1261 VLASEELKTLDRNKLSPSFGMMPSKRSVASGNSQTSQSGYHSDDDTDTTVYSSD 1320
Db 1261 VLASEELKTLDRNKLSPSFGMMPSKRSVASGNSQTSQSGYHSDDDTDTTVYSSD 1320
Qy 1321 EAGLLKMDVDAVAHADSGTTLR 1341
Db 1321 EAGLLKMDVDAVAHADSGTTLQ 1341
RESULT 2
JC1402
protein-tyrosine kinase (EC 2.7.1.112) KDR - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 28-Aug-1998 #text_change 04-Feb-2000
C:Accession: JC1402; I58357
R:Terminator, B.I.; Dougher-Vermazen, M.; Carrion, M.E.; Dimitrov, D.; Armellino, D.C.; Gospo
Biochem. Biophys. Res. Commun. 187, 1579-1586, 1992
A:Title: Identification of the KDR tyrosine kinase as a receptor for vascular endothelial
A:Reference number: JC1402; MUID:93038639; PMID:1417831
A:Accession: JC1402
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-48, 'I', '50-616', 'E', '618-700', 'E', '702-748', 'F', '750-1263', 'I', '1265-1290', 'P', '1292-1
A:Cross-references: EMBL:X61656; NID:931717
Oncogene 6, 1677-1683, 1991
A:Title: Identification of a new endothelial cell growth factor receptor tyrosine kinase.
A:Reference number: I58357; MUID:92019839; PMID:1656371
A:Accession: I58357
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 3-1356 <TER2>
A:Cross-references: GB:L04947; NID:9186674; PIDN:AAAS9459.1; PID:9186675
C:Comment: This enzyme acts as a receptor for vascular endothelial cell growth factor.
C:Genetics:
A:Gene: GDB-KDR
A:Cross-references: GDB:127921; OMIM:191306
A:Map position: 4q12-q12
C:Superfamily: unassigned Sex/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein kin
P:766-790/Domain: transmembrane #status predicted <TM>
F:832-1167/Domain: protein kinase homology <KIN>
F:840-848/Region: protein kinase ATP-binding motif
Query Match 86.6%; Score 6102.5; DB 2; Length 1356;
Best Local Similarity 85.4%; Pred. No. 2.1e-262;
Matches 1160; Conservative 72; Mismatches 111; Indels 15; Gaps 3;
Qy 1 MESKALLAVALWFCVETRAASVGLTGLDPLHPPKLSQDKILITLANTTLQITCRGORDLD 60
Db 1 MESKALLAVALWFCVETRAASVGLTGLDPLHPPKLSQDKILITLANTTLQITCRGORDLD 60
Qy 61 WLWPNQADSRBRLVTBCCGGDSIPCKTLTIPRVVGNNTGAYKCSYRDVDIASTVYVVV 120
Db 61 WLWPNQADSRBRLVTBCCGGDSIPCKTLTIPRVVGNNTGAYKCSYRDVDIASTVYVVV 118
Qy 121 RYRPFPTASVDQHGIVITENKNTKTVIPCRGSIENLVSLCARYPEKRVFVPGNRLS 180
Db 119 QYRPFPTASVDQHGIVITENKNTKTVIPCRGSIENLVSLCARYPEKRVFVPGNRLS 178
Qy 181 WDSIEGFTLPSPYMSIYAGVWFCPEAKINDETYQSIIMYIVVVGRIYDVVILSPHIELSA 240
Db 179 WDSKGGFTIPSPYMSIYAGVWFCPEAKINDETYQSIIMYIVVVGRIYDVVILSPHIELSV 238
Qy 241 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPPGTVAKMFLSTLTIESVT 300
Db 239 GSKVLNCTARTELNVGLDFTWHSPPSKSHHKIYNRDKVPPGTVAKMFLSTLTIDGVT 298

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:30:17 ; Search time 61 Seconds
(without alignments)
6229.941 Million cell updates/sec

Title: US-10-090-183-6
Perfect score: 7046
Sequence: 1 MESKALLAVALWFCVETRAA.....KQVDAAVHADSQTILRSPV 1345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	7046	100.0	1345	7	ABM79009	Abm79009 Murine Flk
2	7020	99.6	1367	6	ABR40197	Abr40197 Murine va
3	6994	99.3	1367	2	AAR31377	Aar31377 Human flk
4	6994	99.3	1367	2	AAR31377	Aar31377 Human flk
5	6994	99.3	1367	2	AAR37504	Aar37504 Murine fl
6	6994	99.3	1367	2	AAR44996	Aar44996 Murine fl
7	6994	99.3	1367	2	AAR67537	Aar67537 Mouse flk
8	6994	99.3	1367	2	AAR97420	Aar97420 Murine fo
9	6994	99.3	1367	2	AAR19875	Aar19875 Murine fl
10	6994	99.3	1367	2	AAY08618	Aay08618 Murine fl
11	6994	99.3	1367	2	ABG70917	Abg70917 Mouse rec
12	6991	99.2	1367	2	AAE25820	Aae25820 Murine re
13	6988	99.2	1367	2	AAR28041	Aar28041 Flk-1. 3/
14	6980	99.1	1367	2	AAR67817	Aar67817 Flk1 rece
15	6967.5	98.9	1373	4	AAR54046	Aar54046 Sequence
16	6127.5	87.0	1356	4	AAY97783	Aay97783 Human VEG
17	6124.5	86.9	1356	4	AAB62475	Aab62475 Human KDR
18	6124.5	86.9	1356	4	AAR97576	Aar97576 Human Flk
19	6124.5	86.9	1356	6	ABR40196	Abr40196 Human vas
20	6124.5	86.9	1356	7	ADBO8954	Adbo8954 Human VEG
21	6124.5	86.9	1356	7	ABM79007	Abm79007 Human VEG
22	6123.5	86.9	1356	5	AAU79426	Aau79426 Human Kin
23	6119.5	86.9	1355	2	AAW80997	Aaw80997 Human rec
24	6119.5	86.9	1356	5	AAU79427	Aau79427 Human Kin
25	6119.5	86.9	1356	5	AAU79430	Aau79430 Human Kin

26	6119.5	86.9	1356	5	AAU79429	Aau79429 Human Kin
27	6102.5	86.6	1356	2	AAW26999	Aaw26999 Novel typ
28	6102.5	86.6	1356	2	AAW59275	Aaw59275 Human KDR
29	4196	59.6	805	2	AAW06196	Aay06196 Anti-angi
30	3851	54.7	731	7	ADB80300	Adb80300 Soluble F
31	3568	50.6	848	2	AAW38240	Aaw38240 VEGF rece
32	3343	47.4	789	2	AAW62488	Aaw62488 Truncated
33	3343	47.4	789	2	AAW68007	Aaw68007 Human sol
34	3327.5	47.2	788	2	AAW47038	Aaw47038 Soluble t
35	3283	46.6	773	7	ADB80302	Adb80302 Soluble h
36	3248	46.1	764	2	AAW69679	Aaw69679 KDR prote
37	3240	46.0	764	5	AAE28915	Aae28915 Human pro
38	3240	46.0	764	6	ABJ26808	Abj26808 VEGF bind
39	3240	46.0	764	7	ADD24478	Add24478 Human ant
40	3240	46.0	764	7	ADD80855	Add80855 Human KDR
41	3233.5	45.9	927	4	AAW97653	Aay97653 Flk-1extr
42	3225	45.8	760	4	AAW62477	Aaw62477 Human VEG
43	3126	44.4	738	3	AAW29639	Aay29639 Human vas
44	3126	44.4	738	3	AAW59302	Aay59302 Human VEG
45	2792	39.6	664	2	AAW62486	Aaw62486 Human sVE

ALIGNMENTS

RESULT 1

ABM79009
ID ABM79009 standard; protein; 1345 AA.

AC ABM79009;

DT 15-JAN-2004 (first entry)

DE Murine Flk-1.

KW Mouse; vascular endothelial growth factor; receptor; Flk-1; vaccine;
genetic immunisation; gene therapy; cytostatic.

OS Mus sp.

PN WO2003073995-A2.

PD 12-SEP-2003.

PF 28-FEB-2003; 2003WO-US006256.

PR 02-MAR-2002; 2002US-00090183.

PA (SRI) SCRIPPS RES INST.

PI Reisfeld RA, Niethammer AG, Xiang R;

DR WPI: 2003-756753/71.

DR N-PSDB; ACF80603.

PT New DNA vaccine for eliciting an immune response against proliferating
endothelial cells comprising a DNA construct operably encoding a VEGF
receptor protein in a carrier, useful for inhibiting tumor growth or
angiogenesis.

PS Claim 3; Fig 6; 56pp; English.

CC The present sequence is the protein sequence of murine Flk-1, an
endothelial growth factor receptor protein. A claimed DNA vaccine
effective for eliciting an immune response against proliferating
endothelial cells comprises a DNA construct operably encoding a VEGF
receptor protein (e.g. Flk-1) in a carrier. The DNA construct may be a
naked DNA construct or incorporated into a plasmid vector or into an
attenuated bacterial vector such as attenuated Salmonella typhimurium.
CC The DNA vaccine is used in claimed methods of inhibiting endothelial cell
proliferation, inhibiting angiogenesis, and inhibiting tumour growth
Sequence 1345 AA;

Query Match		100.0%; Score 7046; DB 7; Length 1345;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MESKALLAVALWFCVETRAASVGLTGDPLHPKLSQKDIILTIANTLTQITCRGQDRLD 60
Db	1	MESKALLAVALWFCVETRAASVGLTGDPLHPKLSQKDIILTIANTLTQITCRGQDRLD 60
Qy	61	WLWPNARSDSERVLVTECGGDSIFCKTLTI PRVGNNDTCAYKCSYRDVDIASTVYVY 120
Db	61	WLWPNARSDSERVLVTECGGDSIFCKTLTI PRVGNNDTCAYKCSYRDVDIASTVYVY 120
Qy	121	RDYRSPFIASVDQHGIVYITENKNTVIFPCRGISINLNVSLCARYPEKEFVDPGNRIS 180
Db	121	RDYRSPFIASVDQHGIVYITENKNTVIFPCRGISINLNVSLCARYPEKEFVDPGNRIS 180
Qy	181	WDSIGFTLPSYMSYAGWFCBAKINDETQSIWYIVVVGRIYDVILSPPEHELSA 240
Db	181	WDSIGFTLPSYMSYAGWFCBAKINDETQSIWYIVVVGRIYDVILSPPEHELSA 240
Qy	241	GEKLVNCTARTLNVLGDTFTHSPBKS SHHKKIVNRDVKPFPCTVAKMFLSTLTIESVT 300
Db	241	GEKLVNCTARTLNVLGDTFTHSPBKS SHHKKIVNRDVKPFPCTVAKMFLSTLTIESVT 300
Qy	301	KSDQGYTCVASSGRMIKRNRTFVRVHTKPIAFSGWKSLVEATVGSQVRI PVKYLSP 360
Db	301	KSDQGYTCVASSGRMIKRNRTFVRVHTKPIAFSGWKSLVEATVGSQVRI PVKYLSP 360
Qy	361	APDIKWYRNGRPIESNTYIMVGDLETIMEVTERDAGNYTILTNPI SMEXQSHMVSIVN 420
Db	361	APDIKWYRNGRPIESNTYIMVGDLETIMEVTERDAGNYTILTNPI SMEXQSHMVSIVN 420
Qy	421	VPOIGEKALISPNDSYQYGTMOQLTCTVYANPLPHIOMYQWLEBACSRPGQTSYAC 480
Db	421	VPOIGEKALISPNDSYQYGTMOQLTCTVYANPLPHIOMYQWLEBACSRPGQTSYAC 480
Qy	481	KEWRHVEDFOGKNIEYTKQYALIEGKNKTVSLVIOANVSALYKCEAINKAGRERV 540
Db	481	KEWRHVEDFOGKNIEYTKQYALIEGKNKTVSLVIOANVSALYKCEAINKAGRERV 540
Qy	541	ISFHVIRGPEITVOPAAQTEQESVSLCTADRNTFENLTWYKLSQATSVHMGESLTPV 600
Db	541	ISFHVIRGPEITVOPAAQTEQESVSLCTADRNTFENLTWYKLSQATSVHMGESLTPV 600
Qy	601	CKNLDAWKLNGTMSNSTNDILVAFQNASLOQGDYVCSAQDKTKRGHCLVKQLIIL 660
Db	601	CKNLDAWKLNGTMSNSTNDILVAFQNASLOQGDYVCSAQDKTKRGHCLVKQLIIL 660
Qy	661	ERNAPMITGNLENQTTIGETIEVTCPASGNPTPHITWFKDNETLVDSGIVLRDGNRNL 720
Db	661	ERNAPMITGNLENQTTIGETIEVTCPASGNPTPHITWFKDNETLVDSGIVLRDGNRNL 720
Qy	721	TIRVRKEDGGLYTQACNVLCARAEFLIEGAQEKTNLEVIILVGTAVIAMFFWLL 780
Db	721	TIRVRKEDGGLYTQACNVLCARAEFLIEGAQEKTNLEVIILVGTAVIAMFFWLL 780
Qy	781	VIVLRTVKRANEGELTKYLSIVMDPELDERCERLPYDASKWPEPRDLKGLPLGR 840
Db	781	VIVLRTVKRANEGELTKYLSIVMDPELDERCERLPYDASKWPEPRDLKGLPLGR 840
Qy	841	GAFQVTEADAFGDKTATCKTAVKMLKEGATHSEHRLMSELKILIHGHNLVNNLL 900
Db	841	GAFQVTEADAFGDKTATCKTAVKMLKEGATHSEHRLMSELKILIHGHNLVNNLL 900
Qy	901	GACTKPGGLMIVTEFCFKNLSTYLRGKNEFVYKSKGARFQGDYVGLSVDLKRR 960
Db	901	GACTKPGGLMIVTEFCFKNLSTYLRGKNEFVYKSKGARFQGDYVGLSVDLKRR 960
Qy	961	LDSITSSQSSAGSGFVEEKSLSVDEEASEELYKDFLTLEHLCYCSFQVAKGMEFLASR 1020
Db	961	LDSITSSQSSAGSGFVEEKSLSVDEEASEELYKDFLTLEHLCYCSFQVAKGMEFLASR 1020

Qy	1021	KCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVY 1080
Db	1021	KCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVY 1080
Qy	1081	TIQSDVMSFGVLLWEIFSLGASYPGVKIDEEFCRLKEGTRMRADPYTTPMYQTMWLD 1140
Db	1081	TIQSDVMSFGVLLWEIFSLGASYPGVKIDEEFCRLKEGTRMRADPYTTPMYQTMWLD 1140
Qy	1141	WHEDPNORPSFSELVHGLNLLQANAQDGKQIVILPMSETLSMEEDSGLSLPTSPVSCM 1200
Db	1141	WHEDPNORPSFSELVHGLNLLQANAQDGKQIVILPMSETLSMEEDSGLSLPTSPVSCM 1200
Qy	1201	EEEEVCDCPFHYDNTAGISHYLQNSKRSRPSVSKTFEDIPLEPEPKVIPDSDQTDGSM 1260
Db	1201	EEEEVCDCPFHYDNTAGISHYLQNSKRSRPSVSKTFEDIPLEPEPKVIPDSDQTDGSM 1260
Qy	1261	VLASEELKTLEDNRNKLSPSFGGMPKSRRESVASEGNSQTSQYQSGYHSDDTDTTVYSSD 1320
Db	1261	VLASEELKTLEDNRNKLSPSFGGMPKSRRESVASEGNSQTSQYQSGYHSDDTDTTVYSSD 1320
Qy	1321	EAGLLAKWDAVAHADSQTTLRSPPV 1345
Db	1321	EAGLLAKWDAVAHADSQTTLRSPPV 1345
RESULT 2		
ABR40197		
ID	ABR40197	standard; protein; 1367 AA.
XX	ABR40197;	
AC	AC	
XX	01-AUG-2003	(first entry)
DE	Murine vascular endothelial growth factor receptor-2.	
XX	Murine; vascular endothelial growth factor receptor-2; cytostatic; angiogenic; antiangiogenic; antiarthritic; antirheumatic; antitense; VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis; angiogenesis.	
OS	Mus musculus.	
XX	WO2003029266-A1.	
PN	10-APR-2003.	
XX	26-SEP-2002; 2002WO-US030734.	
XX	28-SEP-2001; 2001US-00967655.	
PA	(ISIS-) ISIS PHARM INC.	
XX	Bennett CF, Watt AT;	
PI	WPI; 2003-371980/35.	
DR	N-PSDB; ACC71720.	
XX	New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding vascular endothelial growth factor receptor-2 (VEGFR-2), useful for treating a disease/condition associated with VEGFR-2, e.g. cancer.	
PT	Example 13; Page 99-105; 127pp; English.	
PS	The present invention relates to novel antisense oligonucleotides (ACC71728-ACC71750 and ACC80101-ACC80155) targeted to Vascular Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and which inhibit the expression of VEGFR-2. The oligonucleotides are useful in compositions for treating a disease or condition associated with VEGFR-2, such as hyperproliferative disorder, e.g. cancer, a disease or condition involving angiogenesis, or rheumatoid arthritis. The present sequence is murine VEGFR-2	
CC	The present invention relates to novel antisense oligonucleotides (ACC71728-ACC71750 and ACC80101-ACC80155) targeted to Vascular Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and which inhibit the expression of VEGFR-2. The oligonucleotides are useful in compositions for treating a disease or condition associated with VEGFR-2, such as hyperproliferative disorder, e.g. cancer, a disease or condition involving angiogenesis, or rheumatoid arthritis. The present sequence is murine VEGFR-2	

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:30:47 ; Search time 19 Seconds
(without alignments)
3686.019 Million cell updates/sec

Title: US-10-090-183-6
Perfect score: 7046
Sequence: 1 MESKALLAVALWFCVETRAA.....KXVDAVHADSCTTLRSPPV 1345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6998	99.3	1367	1 VGR2_MOUSE	P35918 mus musculus
2	6732	95.5	1343	1 VGR2_RAT	O08775 rattus norv
3	6124.5	86.9	1356	1 VGR2_HUMAN	P35968 homo sapien
4	4810.5	68.3	1348	1 VGR2_COTUA	P52583 coturnix co
5	2746.5	39.0	1363	1 VGR3_MOUSE	P35917 mus musculus
6	2694.5	38.2	1338	1 VGR1_HUMAN	P17948 h vascular
7	2677.5	38.0	1298	1 VGR3_HUMAN	P35916 homo sapien
8	2606	37.0	1336	1 VGR1_RAT	P53767 rattus norv
9	2575	36.5	1333	1 VGR1_MOUSE	P35969 mus musculus
10	1162.5	16.5	1088	1 PGDS_RAT	P20786 rattus norv
11	1162	16.5	1089	1 PGDS_HUMAN	P16234 homo sapien
12	1146	16.3	1089	1 PGDS_MOUSE	P26618 mus musculus
13	1130.5	16.0	1087	1 PGDS_XENLA	P26619 xenopus lae
14	1043.5	14.8	960	1 KIT_CHICK	O08156 gallus gall
15	1019.5	14.5	976	1 KIT_HUMAN	P10721 homo sapien
16	1019	14.5	1106	1 PGDR_HUMAN	P05619 homo sapien
17	1016.5	14.4	975	1 KIT_MOUSE	P05532 mus musculus
18	1013.5	14.4	978	1 KIT_CAPIH	O28317 capra hircu
19	1011	14.3	1097	1 PGDR_RAT	O05030 rattus norv
20	1009	14.3	977	1 KIT_BOVIN	P43481 bos taurus
21	1005	14.3	978	1 KIT_FELCA	P28889 felis silve
22	1003	14.2	806	1 CEK2_CHICK	P18460 gallus gall
23	1002.5	14.2	819	1 FGR1_CHICK	P21804 gallus gall
24	1000.5	14.2	1098	1 PGDR_MOUSE	P05622 mus musculus
25	994	14.1	980	1 KPM5_FELCA	P13369 felis silve
26	992	14.1	821	1 FGR2_MOUSE	P21803 mus musculus
27	990.5	14.1	972	1 KPM5_HUMAN	P07333 homo sapien
28	990	14.1	975	1 KIT_CANFA	O97799 canis fami
29	986	14.0	822	1 FGR1_MOUSE	P16092 mus musculus
30	985	14.0	822	1 FGR1_HUMAN	P11362 homo sapien
31	984	14.0	821	1 FGR2_HUMAN	P21802 homo sapien
32	979	13.9	978	1 KPM5_FSVMD	P00545 feline sarc
33	976.5	13.9	812	1 FGR1_XENLA	P22182 xenopus lae

34	972.5	13.8	823	1 CEK3_CHICK	P18461 gallus gall
35	972	13.8	822	1 FGR1_RAT	O04589 rattus norv
36	964	13.7	813	1 FGR2_XENLA	O03364 xenopus lae
37	961.5	13.6	977	1 KPM5_MOUSE	P09581 mus musculus
38	943.5	13.4	978	1 KPM5_RAT	O00495 rattus norv
39	938.5	13.3	801	1 FGR3_MOUSE	O61851 mus musculus
40	937.5	13.3	806	1 FGR3_HUMAN	P22607 homo sapien
41	937.5	13.3	992	1 FLT3_MOUSE	O00342 mus musculus
42	934	13.3	993	1 FLT3_HUMAN	P36888 homo sapien
43	896	12.7	802	1 FGR4_HUMAN	P22455 homo sapien
44	890.5	12.6	370	1 KIT_FSVHZ	O40048 feline sarc
45	876.5	12.4	808	1 FGR4_MOUSE	O03142 mus musculus

ALIGNMENTS

RESULT 1
VGR2_MOUSE
ID VGR2_MOUSE STANDARD; PRT; 1367 AA.
AC P35918;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VGFRR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
DE 1) (Kinase NYK).
GN KDR OR FLK1 OR FLK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Embryo;
EX MEDLINE=9220880; PubMed=7681362;
RA Millauer B., Witzmann-Voos S., Schnurch H., Martinez R.,
RA Mueller N.P.H., Risaau W., Ullrich A.;
RT "High affinity VEGF binding and developmental expression suggest
RT Flk-1 as a major regulator of vasculogenesis and angiogenesis.";
RL Cell 72:835-846(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Petal liver;
RX MEDLINE=92020984; PubMed=1717995;
RA Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,
RA Lemischka I.R.;
RT "A receptor tyrosine kinase cDNA isolated from a population of
RT enriched primitive hematopoietic cells and exhibiting close genetic
RT linkage to c-kit.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93141255; PubMed=8423988;
RA Oelrichs R.B., Reid H.H., Bernard O., Ziemiecki A., Wilks A.F.;
RT "NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from
RT E10 embryonic neuroepithelium is expressed in endothelial cells of
RT the developing embryo.";
RL Oncogene 8:11-18(1993).
RN [4]
RP SEQUENCE OF 1-15 FROM N.A.
RX MEDLINE=96032749; PubMed=7559454;
RA Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
RA Harber E.;
RT "Cloning and functional analysis of the promoter for KDR/flk-1, a
RT receptor for vascular endothelial growth factor.";
RL J. Biol. Chem. 270:23111-23118(1995).
RN [5]
RP FUNCTION.
RX MEDLINE=93361481; PubMed=8356051;
RA Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;
RT "Fetal liver kinase 1 is a receptor for vascular endothelial growth
RT factor and is selectively expressed in vascular endothelium.";

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OM protein - protein search, using sw model

Run on: July 29, 2004, 13:33:52 ; Search time 51 Seconds
(without alignments)
8321.019 Million cell updates/sec

Title: US-10-090-183-6
Perfect score: 7046
Sequence: 1 MESKALLAVALWFCVETRAA.....KWDAAVHADSGTILRSPPV 1345

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rhodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7040	99.9	1345	11 Q8VCD0	Q8VCD0 mus musculus
2	2913	41.3	1379	13 P79701	P79701 coturnix co
3	2730.5	38.8	1363	11 Q91ZT1	Q91ZT1 rattus norv
4	2666	37.8	1363	4 Q86W07	Q86W07 homo sapien
5	2661.5	37.8	1298	4 Q86W08	Q86W08 homo sapien
6	2639.5	37.5	1327	13 Q8QHL3	Q8QHL3 gallus gall
7	2495.5	35.4	1301	13 Q8UW9	Q8UW9 brachydanio
8	2493	35.4	1302	13 Q8AXB3	Q8AXB3 brachydanio
9	2357.5	33.5	1173	13 Q9PT10	Q9PT10 brachydanio
10	2210.5	31.4	1092	11 Q91ZT0	Q91ZT0 rattus norv
11	1796	25.5	341	11 Q8CD05	Q8CD05 mus musculus
12	1322.5	18.8	346	13 Q42570	Q42570 xenopus lae
13	1172	16.6	287	13 Q42377	Q42377 brachydanio
14	1154.5	16.4	1078	13 Q8AXC8	Q8AXC8 fugu rubrip
15	1150	16.3	1089	11 Q7TSJ3	Q7TSJ3 mus musculus
16	1135	16.1	976	13 Q9W755	Q9W755 brachydanio

17	1135	16.1	1062	13 Q8AXC7	Q8AXC7 fugu rubrip
18	1134	16.1	976	13 Q8JFR5	Q8JFR5 brachydanio
19	1133.5	16.1	1087	13 Q7ZY71	Q7ZY71 xenopus lae
20	1132	16.1	1059	13 Q9DE49	Q9DE49 brachydanio
21	1128.5	16.0	453	11 Q9CW58	Q9CW58 mus musculus
22	1128	16.0	984	13 Q8AXC6	Q8AXC6 fugu rubrip
23	1114.5	15.8	1087	13 Q9PUF6	Q9PUF6 gallus gall
24	1097	15.6	207	6 Q9N112	Q9N112 ovis aries
25	1089	15.5	992	13 Q8AXU0	Q8AXU0 oncorhynch
26	1077.5	15.3	975	13 P79750	P79750 fugu rubrip
27	1075.5	15.3	1474	5 Q8T4M0	Q8T4M0 drosophila
28	1074	15.2	1503	5 Q8T4L8	Q8T4L8 drosophila
29	1065	15.1	1509	5 Q9SP10	Q9SP10 drosophila
30	1064	15.1	1509	5 Q8IPG1	Q8IPG1 drosophila
31	1049.5	14.9	1048	13 P79749	P79749 fugu rubrip
32	1049	14.9	1509	5 Q9VLQ8	Q9VLQ8 drosophila
33	1045	14.8	1461	5 Q8T9F6	Q8T9F6 drosophila
34	1040.5	14.8	977	13 Q98SU2	Q98SU2 dario kerri
35	1037.5	14.7	977	13 Q98SU4	Q98SU4 dario alboi
36	1037	14.7	974	13 Q98SU3	Q98SU3 dario dangi
37	1034.5	14.7	977	13 Q98SU1	Q98SU1 dario nigro
38	1033.5	14.7	977	13 Q918N6	Q918N6 brachydanio
39	1027.5	14.6	986	13 Q8UVR9	Q8UVR9 fugu rubrip
40	1026.5	14.6	979	11 Q8C8K9	Q8C8K9 mus musculus
41	1023.5	14.5	975	11 Q7TS86	Q7TS86 mus musculus
42	1023.5	14.5	1019	13 Q8UVR8	Q8UVR8 fugu rubrip
43	1023	14.5	445	5 Q9U8U8	Q9U8U8 brachiosco
44	1019	14.5	974	11 Q63702	Q63702 rattus ratt
45	1019	14.5	978	11 Q63116	Q63116 rattus norv

ALIGNMENTS

RESULT 1

ID	Q8VCD0	PRELIMINARY;	PRT; 1345 AA.
AC	Q8VCD0;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Kinase insert domain protein receptor.		
GN	KDR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Strausberg R.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.		
DR	EMBL; BC020530; AAH20530.1; -.		
DR	MGB; MGI:96683; Kdr.		
DR	GO; GO:0045155; P:cell fate commitment; IMP.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR001824; RecepttyrknsIII.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	InterPro; IPR008266; Tyr_kinase_AS.		
DR	Pfam; PF00047; Ig; 6.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 2.		
DR	SMART; SM00408; IGc2; 1.		
DR	SMART; SM00219; TyrKc; 1.		
DR	PROSITE; PS50835; IG-LIKE; 5.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.		

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	5390	100.0	5390	15	US-10-090-183-5	Sequence 5, Appli
2	5346	99.2	5470	9	US-09-766-678-1	Sequence 1, Appli
3	5346	99.2	5470	10	US-09-967-655-10	Sequence 10, Appl
4	5336.8	99.0	5406	9	US-09-919-408-5	Sequence 5, Appli
5	5336.8	99.0	5406	9	US-09-872-136-5	Sequence 5, Appli
6	3356	62.3	5842	15	US-10-133-013-269	Sequence 269, App
7	3354.4	62.2	5832	13	US-10-116-802-18	Sequence 18, Appl
8	3317.8	61.6	5830	10	US-09-967-655-3	Sequence 3, Appli
9	3317.8	61.6	5830	16	US-10-159-563-338	Sequence 338, App
10	3317.8	61.6	5830	16	US-10-894-228-7	Sequence 7, Appli
11	3060.8	56.8	4230	15	US-10-262-538-29	Sequence 29, Appl
12	3027.8	56.2	4071	15	US-10-327-414-5	Sequence 5, Appli
13	3027.8	56.2	4071	15	US-10-090-183-1	Sequence 1, Appli
14	3024.6	56.1	4071	15	US-10-022-939-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 247 Seconds
(without alignments)
12110.062 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtccgcagccgata.....tctgcctgtgtgcttatgtt 5390

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
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4: /cgm2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgm2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5346	99.2	5470	2	US-08-443-861-1
2	5346	99.2	5470	3	US-08-193-829B-1
3	5336.8	99.0	5406	1	US-07-813-593-3
4	5336.8	99.0	5406	1	US-07-977-451-5
5	5336.8	99.0	5406	1	US-07-946-507-3
6	5336.8	99.0	5406	1	US-08-252-517-5
7	5336.8	99.0	5406	1	US-07-906-397A-5
8	5336.8	99.0	5406	1	US-08-601-891-5
9	5336.8	99.0	5406	2	US-09-021-324-5
10	5336.8	99.0	5406	5	US-03-872-136B-5
11	5336.8	99.0	5406	5	PCT-US92-02750-7
12	5336.8	99.0	5406	5	PCT-US92-05401-5
13	5336.8	99.0	5406	5	PCT-US92-09893-5
14	3066.8	56.9	4236	1	US-08-810-116-7
15	3066.8	56.9	4236	2	US-07-930-548A-7
16	3024.6	56.1	4071	3	US-09-098-707A-1
17	3024.6	56.1	4071	4	US-09-483-539-1
18	2412.4	44.8	2431	3	US-08-985-526-35
19	1656.8	30.7	2383	1	US-08-232-538-18
20	1656.8	30.7	2383	2	US-08-786-164-18
21	1592.4	29.5	2292	4	US-09-142-956B-1
22	1420	26.3	2264	1	US-08-232-538-16
23	1420	26.3	2264	2	US-08-786-164-16
24	768	14.2	4014	4	US-09-119-014D-5
25	757	14.0	7718	4	US-09-976-594-244
26	716.2	13.3	4195	1	US-08-340-011-1
27	716.2	13.3	4195	3	US-08-901-710-1

28 716.2 13.3 4416 3 US-08-795-430-1 Sequence 1, Appli
29 716.2 13.3 4416 4 US-09-355-700-1 Sequence 1, Appli
30 716.2 13.3 4416 4 US-08-601-132-36 Sequence 36, Appl
31 716.2 13.3 4416 4 US-08-671-573B-36 Sequence 36, Appl
32 716.2 13.3 4425 1 US-08-222-616-31 Sequence 31, Appl
33 716.2 13.3 4425 4 US-08-446-648-31 Sequence 31, Appl
34 716.2 13.3 4425 4 US-09-023-655-889 Sequence 889, App
35 716.2 13.3 4425 4 US-09-982-610-31 Sequence 31, Appl
36 716.2 13.3 4425 5 PCT-US95-04228-31 Sequence 31, Appl
37 716.2 13.3 4795 1 US-08-340-011-3 Sequence 3, Appli
38 716.2 13.3 4795 3 US-08-901-710-3 Sequence 3, Appli
39 716.2 13.3 9108 4 US-08-446-648-45 Sequence 45, Appl
40 716.2 13.3 9108 4 US-09-982-610-45 Sequence 45, Appl
41 716.2 13.3 9108 5 PCT-US95-04228-45 Sequence 45, Appl
42 298.8 5.5 6827 1 US-08-222-616-17 Sequence 17, Appl
43 298.8 5.5 6827 4 US-08-446-648-17 Sequence 17, Appl
44 298.8 5.5 6827 4 US-09-982-610-17 Sequence 17, Appl
45 298.8 5.5 6827 5 PCT-US95-04228-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-443-861-1
; Sequence 1, Application US/08443861
; Patent No. 5851999
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Risau, Werner
; APPLICANT: Millauer, Birgit
; APPLICANT: Gazit, Aviv
; APPLICANT: Levitzki, Alex
; TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
; TITLE OF INVENTION: Endothelial Growth Factor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,861
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,829
; FILING DATE: 09-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-060
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212)869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 286..4386

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 8373 Seconds
(without alignments)
19223.355 Million cell updates/sec

Title: US-10-090-183-5
Perfect score: 5390
Sequence: 1 cgtgtccgcagccggata.....tctgctgtgtgttatgtt 5390

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_nam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rtd:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106.6	39.1	2612	11 AK031739	AK031739 Mus muscu
2	1566.8	29.1	3176	11 AK054510	AK054510 Mus muscu
3	816.2	15.1	868	14 CA979203	CA979203 AGENCOURT
4	765.6	14.2	809	13 BU709245	BU709245 UI-M-EVO-

5	751.8	13.9	816	12 BI081886	BI081886 602877109
6	750.6	13.9	835	12 BI731060	BI731060 603351683
7	730.2	13.5	896	14 CB849137	CB849137 MRA-0816
8	716.2	13.3	948	13 BO714332	BO714332 AGENCOURT
9	712	13.2	724	13 BO572695	BO572695 UI-M-PD0-
10	702.4	13.0	748	14 CF539944	CF539944 UI-M-EX0-
11	685.4	12.7	857	14 CD107886	CD107886 AGENCOURT
12	674	12.5	751	14 CA512955	CA512955 UI-R-FJ0-
13	658.2	12.2	1067	12 BM925760	BM925760 AGENCOURT
14	653	12.1	786	14 CA463143	CA463143 AGENCOURT
15	636.4	11.8	697	12 BM963389	BM963389 UI-M-EQ0-
16	630.2	11.7	729	12 BG863384	BG863384 602797030
17	629.6	11.7	1195	9 AL550235	AL550235 AL550235
18	626	11.6	953	13 BQ946333	BQ946333 AGENCOURT
19	609.2	11.3	656	10 BB577273	BB577273 BB577273
20	600	11.1	600	14 CA527179	CA527179 8032-85 M
21	586.8	10.9	924	10 BF098937	BF098937 601750434
22	580.2	10.8	689	9 AA122701	AA122701 m038d07.r
23	574	10.6	3751	29 AY404031	AY404031 Homo sapi
24	570	10.6	3559	29 AY404032	AY404032 Pan trogl
25	567.2	10.5	659	9 AA033284	AA033284 m140d09.r
26	563.2	10.4	675	10 BE287063	BE287063 601091038
27	554.6	10.3	645	10 BE3336067	BE3336067 u884a10.y
28	527.4	9.8	553	12 BM248779	BM248779 K0822C02-
29	526.6	9.8	627	10 BF302717	BF302717 602032587
30	526	9.8	763	10 BF784985	BF784985 602110935
31	522.2	9.7	723	14 CD806166	CD806166 UI-M-GW0-
32	509.4	9.5	563	14 CB608012	CB608012 AMGNNUC.S
33	503	9.3	709	9 AI325028	AI325028 m038d07.x
34	502.6	9.3	556	14 CB613414	CB613414 AMGNNUC.M
35	498.2	9.2	3754	29 AY404033	AY404033 Mus muscu
36	479.4	8.9	623	10 BF087145	BF087145 PM1-HT045
37	470.6	8.7	701	13 BQ603967	BQ603967 MI-P-CP1-
38	461	8.6	919	10 BE916077	BE916077 601666379
39	451.6	8.4	974	12 BI599221	BI599221 603250251
40	448.6	8.3	711	14 CF109220	CF109220 Shultzomi
41	444	8.2	807	14 CD656643	CD656643 AGENCOURT
42	441.4	8.2	443	13 BY544133	BY544133 BY544133
43	437.2	8.1	477	14 W85664	W85664 mf42a11.r1
44	436.2	8.1	765	12 BI823988	BI823988 603039184
45	435.4	8.1	487	14 CB726482	CB726482 AMGNNUC.N

ALIGNMENTS

RESULT 1
AK031739
LOCUS
DEFINITION
AK031739 2612 bp mRNA linear HTC 18-SRP-2003
Mus musculus 14 days embryo thymus cDNA, RIKEN full-length enriched
library, clone:6130401C07 product:kinase insert domain protein
receptor, full insert sequence.

ACCESSION
AK031739
VERSION
AK031739.1 GI:26327576
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Carninci, P. and Hayashizaki, Y.
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 1229 Seconds
(without alignments)
18631.235 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtccgcagccggata.....ctgtgtgtgtgtgtatggt 5390

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002as:*
- 7: Geneseq2003as:*
- 8: Geneseq2003bs:*
- 9: Geneseq2003cs:*
- 10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5390	100.0	5390	9	ACF80603
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4	5336.8	99.0	5406	2	AAQ53504
5	5336.8	99.0	5406	2	AAQ79070
6	5336.8	99.0	5406	2	AAQ81014
7	5336.8	99.0	5406	2	AAQ72119
8	5336.8	99.0	5406	6	AB555046
9	5335.2	99.0	5406	2	AAQ35251
10	5331.6	98.9	5470	2	AAQ64049
11	5330.4	98.9	5406	2	AAQ29957
12	5322.8	98.8	5404	2	AAQ73735
13	5322.8	98.8	5404	2	AAQ77516
14	5074.8	94.2	5363	6	AAQ42485
15	4259	79.0	5892	9	AD58183
16	3354.4	62.2	5832	8	ACH03813
17	3317.8	61.6	5830	7	ACC71713
18	3316.2	61.5	5830	9	ADD08953
19	3081.2	57.2	4225	4	AAQ83308
20	3066.8	56.9	4236	2	AAQ34763
21	3027.8	56.2	4071	6	ABV78213
22	3027.8	56.2	4071	6	AB35789
23	3027.8	56.2	4071	6	ABX10032

ALIGNMENTS

RESULT 1

ACF80603

ID ACF80603 standard; cDNA; 5390 BP.

XX

AC ACF80603;

DT 15-JAN-2004 (first entry)

XX

DE Murine Flk-1 coding sequence.

XX

KW Mouse; vascular endothelial growth factor; receptor; Flk-1; vaccine;
KW genetic immunisation; gene therapy; cytostatic; gene; ss.

OS Mus sp.

XX

FT Key Location/Qualifiers

FT CDS 208..4347

FT /tag= a

FT /product= "Mouse Flk-1"

XX

PN WO2003073995-A2.

XX

PD 12-SEP-2003.

XX

PF 28-FEB-2003; 2003WO-US006256.

XX

PR 02-MAR-2002; 2002US-00090183.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Reisfeld RA, Niethammer AG, Xiang R;

XX

DR WPI; 2003-756753/71.

XX

DR P-PSDB; ABM79009.

XX

PT New DNA vaccine for eliciting an immune response against proliferating

XX

PT endothelial cells comprising a DNA construct operably encoding a VEGF

XX

PT receptor protein in a carrier, useful for inhibiting tumor growth or

XX

PS Claim 9; Fig 5; 56pp; English.

XX

CC The present sequence is the coding sequence for murine Flk-1, an

XX

CC endothelial growth factor receptor protein. A claimed DNA vaccine

XX

CC effective for eliciting an immune response against proliferating

XX

CC endothelial cells comprises a DNA construct operably encoding a VEGF

CC receptor protein (e.g. Flk-1) in a carrier. The DNA construct may be a
 CC naked DNA construct or incorporated into a plasmid vector or into an
 CC attenuated bacterial vector such as attenuated *Salmonella typhimurium*.
 CC The DNA vaccine is used in claimed methods of inhibiting endothelial cell
 CC proliferation, inhibiting angiogenesis, and inhibiting tumour growth
 XX
 SQ Sequence 5390 BP; 1397 A; 1297 C; 1422 G; 1274 T; 0 U; 0 Other;

Query Match		100.0%;	Score 5390;	DB 9;	Length 5390;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 5390;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTGTGTCCTCCGACGCGGATACCTGCTGACCGGATTCGCGGACACCCGCTGACGCGCG	60		
Db	1	CTGTGTCCTCCGACGCGGATACCTGCTGACCGGATTCGCGGACACCCGCTGACGCGCG	60		
Qy	61	GCTGAGCCAGGCGCGGTCGCCCGCTCTCCCGGCTCTGCGCTGCGGCGGCATAC	120		
Db	61	GCTGAGCCAGGCGCGGTCGCCCGCTCTCCCGGCTCTGCGCTGCGGCGGCATAC	120		
Qy	121	CGCTCTGTGACTTCTTTGCGGCGCAGGACGAGAGAGTCTGCTGAGAACTGG	180		
Db	121	CGCTCTGTGACTTCTTTGCGGCGCAGGACGAGAGAGTCTGCTGAGAACTGG	180		
Qy	181	GCTCTGTGCGCAGGCGGAGTGCAGATGAGAGCAAGGCTGCTGAGTGTGCTCTG	240		
Db	181	GCTCTGTGCGCAGGCGGAGTGCAGATGAGAGCAAGGCTGCTGAGTGTGCTCTG	240		
Qy	241	TGTTCTGTGCGGAGCCGAGCGGCTCTGTGGGTTTGAATGCGGATTTCTCCATCC	300		
Db	241	TGTTCTGTGCGGAGCCGAGCGGCTCTGTGGGTTTGAATGCGGATTTCTCCATCC	300		
Qy	301	CCCAAGCTCAGCACACAGAAACATACAGCAATTTTGGCAATAACACCTTCAGATT	360		
Db	301	CCCAAGCTCAGCACACAGAAACATACAGCAATTTTGGCAATAACACCTTCAGATT	360		
Qy	361	ACTTGACGGGACAGCGGACCTGACTGGCTTTGGCCCAATGCTCAGGTGATTCGAG	420		
Db	361	ACTTGACGGGACAGCGGACCTGACTGGCTTTGGCCCAATGCTCAGGTGATTCGAG	420		
Qy	421	GAAAGGTTATGCTGAATGCGGCGGTGTGACAGTATCTCTGCAAAACACTCACC	480		
Db	421	GAAAGGTTATGCTGAATGCGGCGGTGTGACAGTATCTCTGCAAAACACTCACC	480		
Qy	481	ATTCAGGGTGTGGAATGATACCTGAGGCTACAGTCTGTGACCGGAGCTGAC	540		
Db	481	ATTCAGGGTGTGGAATGATACCTGAGGCTACAGTCTGTGACCGGAGCTGAC	540		
Qy	541	ATAGCTTCCACTGTTATGCTATGTTGAGATTTACAGATCACCATTCTGCTGTC	600		
Db	541	ATAGCTTCCACTGTTATGCTATGTTGAGATTTACAGATCACCATTCTGCTGTC	600		
Qy	601	AGTGACAGCATGTCATGCTGATCATCACCGAGAAACAGAAACAACTGTTGATCCCC	660		
Db	601	AGTGACAGCATGTCATGCTGATCATCACCGAGAAACAGAAACAACTGTTGATCCCC	660		
Qy	661	TGCGGAGGGTTCGATTTCAACCTCAATGTGCTCTTTGCGTAGGTATCCAGAAAGAGA	720		
Db	661	TGCGGAGGGTTCGATTTCAACCTCAATGTGCTCTTTGCGTAGGTATCCAGAAAGAGA	720		
Qy	721	TTTGTTCGAGTGAACAGAAATTTCTGCGGACGAGATAGGCTTTTACTCTCCCACT	780		
Db	721	TTTGTTCGAGTGAACAGAAATTTCTGCGGACGAGATAGGCTTTTACTCTCCCACT	780		
Qy	781	TACATGATCAGCTATGCGGCAATGCTTCTGTGAGGCAAGATCAATGATGAACCTAT	840		
Db	781	TACATGATCAGCTATGCGGCAATGCTTCTGTGAGGCAAGATCAATGATGAACCTAT	840		
Qy	841	CAGTCTATCATGATAGTGTGTTGATGATATAGGATTTATGATGATTTCTGAGC	900		
Db	841	CAGTCTATCATGATAGTGTGTTGATGATATAGGATTTATGATGATTTCTGAGC	900		
Qy	901	CCCCGCGATGAAATGAGCTATCTGCGGAGAAACCTTGCTTTAAATTTGTACAGCGAGA	960		

Db	901	CCCCGCGATGAAATGAGCTATCTGCGGAGAAACCTTGCTTTAAATTTGTACAGCGAGA	960
Qy	961	ACAGAGCTCAATGTGGGCTTGATTTACCTGGCACTCTCCACCTTCAAGTCTCATCAT	1020
Db	961	ACAGAGCTCAATGTGGGCTTGATTTACCTGGCACTCTCCACCTTCAAGTCTCATCAT	1020
Qy	1021	AAGAAGATTGTAAACCGGGATGTGAACCCCTTTCTGCGACTGTGGCGAAGATGTTTG	1080
Db	1021	AAGAAGATTGTAAACCGGGATGTGAACCCCTTTCTGCGACTGTGGCGAAGATGTTTG	1080
Qy	1081	AGCACTTGTACATAGAAAGTGTGACCAAGAGTGACCAAGGGGATATACCTGTGTAGCG	1140
Db	1081	AGCACTTGTACATAGAAAGTGTGACCAAGAGTGACCAAGGGGATATACCTGTGTAGCG	1140
Qy	1141	TCCAGTGGACGGATGATCAAGAGAAATAGAAATTTGTCCGAGTTCAACAAGCCCTTTT	1200
Db	1141	TCCAGTGGACGGATGATCAAGAGAAATAGAAATTTGTCCGAGTTCAACAAGCCCTTTT	1200
Qy	1201	ATTGCTTTCCGTAGTGGGATGAAATCTTTGTGAGAGCCACAGTGGGCACTCAAGTCCGA	1260
Db	1201	ATTGCTTTCCGTAGTGGGATGAAATCTTTGTGAGAGCCACAGTGGGCACTCAAGTCCGA	1260
Qy	1261	ATCCCTGTGAGTATCTCAGTTACCCAGCTCTCTGATATCAAAATGTTACAGAAATGGAAG	1320
Db	1261	ATCCCTGTGAGTATCTCAGTTACCCAGCTCTCTGATATCAAAATGTTACAGAAATGGAAG	1320
Qy	1321	CCCATTTAGTCCAACTACACATGATTTGTGGCGATGAATCAACCATATGGAAGTGAAT	1380
Db	1321	CCCATTTAGTCCAACTACACATGATTTGTGGCGATGAATCAACCATATGGAAGTGAAT	1380
Qy	1381	GAAAGAGTACAGGAAACTACACGGTCACTCTCACCACCCCAATTTCAATGAGAAACAG	1440
Db	1381	GAAAGAGTACAGGAAACTACACGGTCACTCTCACCACCCCAATTTCAATGAGAAACAG	1440
Qy	1441	AGCCACATGTTCTCTGTTGTAATGTCCTCCACCCAGATCGGTGAGAAAGCCTTGATC	1500
Db	1441	AGCCACATGTTCTCTGTTGTAATGTCCTCCACCCAGATCGGTGAGAAAGCCTTGATC	1500
Qy	1501	TGCGCTATGATTCCTACCAAGTGGGACCATGAGACATTTGACATGACAGCTTACGCC	1560
Db	1501	TGCGCTATGATTCCTACCAAGTGGGACCATGAGACATTTGACATGACAGCTTACGCC	1560
Qy	1561	AACCTTCCCTGACCACTCAGTGTGTAATGTCCTCCACCCAGATCGGTGAGAAAGCCTTGATC	1620
Db	1561	AACCTTCCCTGACCACTCAGTGTGTAATGTCCTCCACCCAGATCGGTGAGAAAGCCTTGATC	1620
Qy	1621	CCCGGCCAAACAGCCGTTATGCTTTGTAAGATGAGACACCTGAGGATTTCCAGGGG	1680
Db	1621	CCCGGCCAAACAGCCGTTATGCTTTGTAAGATGAGACACCTGAGGATTTCCAGGGG	1680
Qy	1681	GGAAACAGATCGAAGTCAACCAAAACCAATATGCTTCAATGAGGAAACCAAACT	1740
Db	1681	GGAAACAGATCGAAGTCAACCAAAACCAATATGCTTCAATGAGGAAACCAAACT	1740
Qy	1741	GTAAGTACGCTGCTCATCCAGCTGCAACCTGTCAGCTTGTACAAATGTGAAGCAATC	1800
Db	1741	GTAAGTACGCTGCTCATCCAGCTGCAACCTGTCAGCTTGTACAAATGTGAAGCAATC	1800
Qy	1801	ACCAAGCGGACGAGGAGAGAGGCTCATCTCTTCCATGATCAGGGGCTCTGAAATTT	1860
Db	1801	ACCAAGCGGACGAGGAGAGAGGCTCATCTCTTCCATGATCAGGGGCTCTGAAATTT	1860
Qy	1861	ACTGTGCAACTGCTGCGCCAGGAGAGAGGCTCATCTCTTCCATGATCAGGGGCTCTGAAATTT	1920
Db	1861	ACTGTGCAACTGCTGCGCCAGGAGAGAGGCTCATCTCTTCCATGATCAGGGGCTCTGAAATTT	1920
Qy	1921	GACAGAAATACGTTTGAAGAACTCAGCTGGTACAGCTTGGCTCAGGCAACATCGGTC	1980
Db	1921	GACAGAAATACGTTTGAAGAACTCAGCTGGTACAGCTTGGCTCAGGCAACATCGGTC	1980
Qy	1981	CAGTGGCGAATCACTCACAACCTTTGCAAGAACTTGGATGCTCTTTGGAACCTGAAT	2040

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 10:44:22 ; Search time 13494 Seconds
(without alignments)
17312.802 Million cell updates/sec

Title: US-10-090-183-5

Perfect score: 5390

Sequence: 1 ctgtgtccgcagccggata.....tctgcgtgtgcttatgtt 5390

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_or.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_ro.*

26: em_sts.*

27: em_un.*

28: em_vl.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5366.2	99.6	5391	10 MMFLK1	X59397 Mouse Plk-1
2	5346	99.2	5470	6 AR068047	AR068047 Sequence
3	5346	99.2	5470	6 AR125598	AR125598 Sequence
4	5346	99.2	5470	10 MMFLK1M	X70842 M.musculus
5	5336.8	99.0	5406	6 AR005213	AR005213 Sequence
6	5336.8	99.0	5406	6 AR071705	AR071705 Sequence
7	5336.8	99.0	5406	6 I25171	I25171 Sequence 5
8	5336.8	99.0	5406	6 I40602	I40602 Sequence 5
9	5279.6	98.0	5464	10 BC020530	BC020530 Mus muscu
10	4657.2	86.4	4790	10 S53103	S53103 NYK/PLK-1
11	4259	79.0	5892	10 RN093306	RN093306 Rattus norv
12	3317.8	61.6	5830	6 AX743112	AX743112 Sequence
13	3317.8	61.6	5830	9 AF035121	AF035121 Homo sapi
14	3081.2	57.2	4225	6 AX133539	AX133539 Sequence
15	3066.8	56.9	4236	6 AR030758	AR030758 Sequence
16	3060.8	56.8	4230	9 HSGPRTK	H61656 H.sapiens m
17	3060.8	56.8	4230	9 HUMKDRZ	L04947 Homo sapien
18	3027.8	56.2	4071	6 AX481483	AX481483 Sequence
19	3027.8	56.2	4071	9 AF063658	AF063658 Homo sapi
20	3026.2	56.1	4044	6 AX481480	AX481480 Sequence
21	3024.6	56.1	4071	6 AR142803	AR142803 Sequence
22	3024.6	56.1	4071	6 AR201382	AR201382 Sequence
23	3024.6	56.1	4071	6 BD132942	BD132942 Human rec
24	2728	50.6	4016	10 RN093307	RN093307 Rattus norv
25	2412.4	44.8	2431	6 AR100641	AR100641 Sequence
26	2412.4	44.8	2431	6 E34072	E34072 Carrier/DNA
27	1904.8	35.3	5390	5 CCQUEK1	X83288 C.coturnix
28	1753.8	32.5	2555	6 A64406	A64406 Sequence 19
29	1656.8	30.7	2383	6 AR030850	AR030850 Sequence
30	1656.8	30.7	2383	6 I82809	I82809 Sequence 18
31	1621.6	30.1	3009	6 AX060542	AX060542 Sequence
32	1592.4	29.5	2292	6 AR194072	AR194072 Sequence
33	1581.4	29.3	2281	6 AX133543	AX133543 Sequence
34	1420	26.3	2264	6 AR030848	AR030848 Sequence
35	1420	26.3	2264	6 I82807	I82807 Sequence 16
36	1279.2	23.7	221665	2 AC134903	AC134903 Mus muscu
37	810.6	15.0	4617	5 CCQUEK2	X83287 C.coturnix
38	768	14.2	4014	6 AR397397	AR397397 Sequence
39	768	14.2	4017	6 AX481481	AX481481 Sequence
40	768	14.2	4017	9 AF063657	AF063657 Homo sapi
41	768	14.2	7680	9 HSFLT	X51602 Human flt m
42	727.8	13.5	2619	5 S65205	S65205 endothelial
43	727	13.5	4272	5 AB065372	AB065372 Gallus ga
44	720.6	13.4	5284	10 MUSRTKA	L07296 Mus musculu
45	717.8	13.3	3897	6 AX481482	AX481482 Sequence

ALIGNMENTS

RESULT 1

MMFLK1

LOCUS MMFLK1

DEFINITION Mouse Plk-1 mRNA for a tyrosine kinase receptor.

ACCESSION X59397

VERSION X59397.1 GI:50976

KEYWORDS Plk-1 gene; tyrosine kinase receptor.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 5391)

AUTHORS Matthews,W., Jordan,C.T., Gavin,M., Jenkins,N.A., Copeland,N.G. and Lemischka,I.R.

TITLE A receptor tyrosine kinase cDNA isolated from a population of

5391 bp mRNA linear ROD 06-NOV-1991